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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Best Local Similarity 100.0%;
Matches 469; Conservative (
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01-JUL-1997
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MEDLINE=97258620; PubMed=9104814;

Lee S.Y., Lee S.Y., Choi Y.;

"TRAF-interacting protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes that inhibits TRAF2-mediated NF-kappaB activation.";

J. Exp. Med. 185:1275-1285(1997).

-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                EMBL; U77845; AAB52993.1; -.
Interpro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 469 AA;
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 61 KLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS 120
                          MPIRALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIIN
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Last sequence update)
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SMART; SM00184; RING; 1.
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TRAF INTERACTING PROTEIN.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE 4
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                                              LQQALGKAEMLCSTLKKOMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV
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RX MEDLINE-21085660; PubMed-11217851;
RX MEDLINE-21085660; PubMed-11217851;
RX MEDLINE-21085660; PubMed-11217851;
RX Marai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Arakawa T., Saito R.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsud Y., Nishaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nishaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nishaido I., Wagner L., Washio T.,
RA Kuehl P., Lewis S., Matsuo Y., Nishaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Bringa N., Carninci P., de Bonaldo M.F.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
Penctional anotation of a fill-leggth mouse CDNA Collection ".
Query Match 78.5
Best Local Similarity 79.1
Matches 370; Conservative
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O1-DEC-2001 (TrEMBLrel. 19,
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-i-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AK012948; BAB28567.1; -.
EMBL; AK012786; BAB28469.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE 4
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
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Last sequence update)
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Score 1870.5; DB 11;
Pred. No. 9.2e-94;
2; Mismatches 55; 1
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Lee S.Y., Lee S.Y., Choi Y.;

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SEQUENCE 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV
                                                                                                                                            LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV
                                                                                                                                                                          KLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVLKKVHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLN
                                                                                         EEMIRDMGVGQSAVEQLAVYCVSLKK
                                                                                                                                  LQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSEV
                                                                                                                                                                                                                                                        188;
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                  2001) to the AAH06929.1;
                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                         25584 MW;
                                                                                                                                                                                                                                                                 40.1%;
91.3%;
 10,
10,
                                                                                                                                                                                                                                                      Score 955; DB
Pred. No. 1.2e
8; Mismatches
                                                                                                                                                                                                                                                       8;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                         412291C205C43071
                                                                                                            206
                                                                                                                                                                                                                                                                 955; DB 11;
No. 1.2e-44;
                                         433
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                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
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                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                              Murinae;
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Best Local
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                 Q95SS5;
Q95SS5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
GH03577P.
CG5140.
Drosophila
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elgar G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cottage
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                                                                                                                      372
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                                                                                                                                                                                                                                          SELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLE--SPAP
                                                                                                                                                                                                                                                                                                                 LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV
                                                                                                                                      RTGFDGLGGRTKFIQPTDTVMIRPLPVKPK
                                                                                                                                                                          KKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVV
                                                                                                                                                                                              PQNSRVSKASCLHPPSGNEDIDLNMTYDVTTP
                                                                                                                                                                                                      ----VEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVP
                                                                                                                                                                                                                                                                              EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY
                                                                                                                                                                                                                                                                                                       LQKDVMEKEKLCSALRTQMTYLESQHNDTRAAKEEVRRLRIKMKTFESLDVVLQGQRAEV
                                                                                                                                                                                                                                                                                                                                           RLYFDVGLDDSSVGDPESLQNELDRVKVNFSSKERDWREKQKAMDDLMETVELQRKALEN
                                                                                                                                                                                                                                                                                                                                                    LELTKARDDMKSLQNDLTNAEKEISSLKKKVEFLQEALSTPTRTNEALGRLFFERCGAAP
                                                                                                                                                                                                                                                                   ESMITDMGIGQAAVEQLSIYCISLKKEYDNLKGGLKSSNEMCEKLKREVLTSNNKLHKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
197; Conserv
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melanogaster (Fruit 1
Metazoa; Arthropoda;
                                     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10025966;
rk M., Hawker K.,
                                                                                                                                                                                                                                                                                                                                                                                                                          38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               49201 MW;
                                                                                                                                                        ------DSVVILLRTKYKNLVSNQGK
                                     19,
19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                  76;
                                    Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 925; DB 13;
Pred. No. 9.8e-43;
                                                                        PRT;
          fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A8C31AAA4216E8C2 CRC64;
 Tracheata;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                      401
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 Hexapoda;
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                                     update)
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 Insecta;
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Best Local Similarity 25.1
Matches 113; Conservative
                                                                                                                                                          Q9V8D7;
01-MAY-2000
01-MAY-2000
01-DEC-2001
CG5140 PROTE
MEDLINE-20196006; PubMed-10731132; Adams M.D., Celniker S.E., Holt R. Amanatides P.G., Scherer S.E., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawez C., Dorsett V., Farfan D., Frise E., George R. Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY066510; AAL28158.1; -.

SEQUENCE 435 AA; 48455 MW; OBFFOAC81DD9416E CRC64;
                                      SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                            Pterygota; Neoptera; Endoptephydroidea; Drosophilidae;
                                                                                                                                   Drosophila
                                                                                                                                                 CG5140
                                                                                                                                                                                                                             Q9V8D7
                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                              NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                KSH-SPIQDVPKKICKGPRKESQLSLGGQSCAG---
                                                                                                                                                                                                                                                                                                                                                                                                                   RLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYE-----
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                                                                                                                                                                                                                                                                                               PRLLLGSSSSSALTATTGSNFVYNGMGGSEK
                                                                                                                                                                                                                                                                                                                     PKRPRSESSCSKDVVRTG----FDGLGGRTK
                                                                                                                                                                                                                                                                                                                                                    KSKISPIKGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALG
                                                                                                                                                             PROTEIN
                                                                                            melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musoa; Drosophilidae; Drosophila.
                                                                                                                                                                        (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.2%;
                                                                                                                                                                          13,
13,
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                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
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Pred. No. 1.6e-08;
2; Mismatches 161;
 Li P.W.,
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             Evans
  Hoskins
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             Ά.,
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 R.A.,
 Gocayne J. A., Galle
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                                                                                                           Muscomorpha;
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 .D.,
R.F.,
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RA Ballew R.M. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Liai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menson D.R., Walson K.A., Nixon K., Nuzskern D.R., Pacleb J.M.,
RA Melson D.R., Welson K.A., Nixon K., Nuzskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stappson M., Skupski M.P., Smith T.,
RA Welson D.R., Welson K., Meinstock G.M., Weissenbach J.,
RA Weillams S.M., Woodage T., Weilscon M., Stupski M.P., Smith T.,
RA Weilson R., Poctor C., Turner R., Venter E., Wang A.H., Wang X.,
RA H., Weng X., Weilsch M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Erns: L., Raft Ing.
RA Spier F., Shen H., Zhong W., Lin, Sheng L.,
RA Shens R., Frector C., Tu
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                                        LTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPS
                                                                                                                                                                          ----EADPHVLANWVSTLKRELRQCESKKTELRNVVKVVQNDLRKEIELKRYAHNIPNVV
                                                                                                                                                                                                                  MGVGQSAVEQLAVYCVSLKKEYENLK----EARKASGEVADKLRKDLFSSR------
                                                                                                                                                                                                                                                                    KKDFLISSYVEQIGVLKSDAHVVDGLRKENKTLKSQIQSMEGISAILAAGSADADRLLKN
                                                                                                                                                                                                                                                                                                              KAEMLCSTLKKOMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEVEEMIRD
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                                                                                  FIIDMCSFDCSKLEERVSHLESDLYQAQEKLQAFENKTAYLDSPNASCGLNSNILALKRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%; Score 286.5; DB 5; 24.3%; Pred. No. 3.2e-08; tive 82; Mismatches 161;
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                                                                                                                               -QAKL---ELKSAQKDLQSA----DKEIMSLKKK
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01-0CT-2000 (T)
01-DEC-2001 (T)
PUTATIVE RING
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Q9M143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenB
-:- SIMILARITY: CONTAINS 1 RING-TYPE
EMBL; AL161491; CAB80936.1; --
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; Zf-C3HC4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger.
SEQUENCE 506 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AT4G01270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                           RDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKE------
                                                                               KSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRRPSF
                                                                                                           ARSSEKLEKALEKIEKLKKRMRELELITEERENRALRDINVSK---KCSYTEVSEPAIES
                                                                                                                                   S-AVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLEL
                                                                                                                                                               ASLKLVSDLSLEEDDVLKLALLGNNAKTKDTIDTLVKSLVIRNRSYKELLAKCNQLGRGE
                                                                                                                                                                                         KYLEQQQDETKQAQE--EAGRLRSKMKTMEQIELLLQS-----QLPEVEEMIRDMGVGQ
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VSRTDSVIDVDDDYVPETNTSGIRDWNTNIEEKGDNSMVKDIKFNIRKDPTSSVSPYSNG
                                                      MSSFRMLSSDNK - -
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
NG ZINC FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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21.5%;
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the EMBL/GenBank/DDBJ dat
" " bTNG-TYPE ZINC FINGER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 204.5; DB 1
Pred. No. 0.00096;
                                                      ·VEKISTPPGKLEEKDGFTIQGSC-----LRGREDSF
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043241;
01-JUN-1998
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MEDLINE-97442456; PubMed-9295333;

MISUMI Y., Schda M., Yano A., Fujlwara T., Ikehara Y.;

MISUMI Y., Schda M., Yano A., Fujlwara T., Ikehara Y.;

Molecular Characterization of GCP170, a 170-kDa Protein Associated with the Cytoplasmic Face of the Golgi Membrane.";

J. Biol. Chem. 272:23851-23858(1997).

EMBL; D63997; BAA23661.1; -.

EMBL; D63997; BAA23661.1; -.
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Homo sapiens (Human).
Homo sapiens (Human).
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 VVDVFL
                         KLDTFL
                                                  RPTETQSEQ-
                                                                                                   \tt QGAPQEPEQLPPAAQAGDGQPAAPDGGARPDGARVSVLVDAAGASHCQPCAPGGSRRPTR
                                                                                                                             CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAIL------
                                                                                                                                                                               LKLRRPSFRDDIDLNATFDVDTP----PARPSSSQHGYYEKLCLEKSHSPIQDVPKKI
                                                                                                                                                                                                         EMAQEDLSMTQKDKFMLQAKVSELKNNMKTLLQQNQQL---
                                                                                                                                                                                                                                 DOAKLELKSAOKDLOSADKEIMSLKKKL-TMLQETLNLPPVASETVDRLVLESPAPVEVN
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                                                                         PRSESSCSKDVVRTGFDGLGGRTKFTQPTDTVMIRPLPVKPKTKVKQRVRVKTVPSLFQA
                                                                                                                                                     LDLRRG--QDEKGAESAGQLFQPCHAHQDPGLPSSRL----
                                                                                                                                                                                                                                                            LSKQPVGNQEMENLKWEVDQKEREIQSLKQQLDLTEQQG----RKELEGLQQLLQNVKSEL
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03; Conservative
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                                                   GFQRRAGRVTAVDSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 188; DB 4;
Pred. No. 0.025;
7; Mismatches 194
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RESULT 12
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Q9DGD5
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Best Local S
Matches 76
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                                                                                                                                                                                                                                                                                   1195
                                                                                                                                                                                                                                                                                                                                    1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0193; MYOSĪNHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
SPROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.; "cDNA cloning and characterization of the complete primary str myosin heavy chain from whitz croaker fast skeletal muscle."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB039672; BAB12571.1; -. HSSP; P13538; 2MIS.
                                                                             1419
                                                                                                                             1364
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Pfam; PF00063; myosin_head; 1.

Pfam; PF02736; myosin_N; 1.

Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Acanthomorpha; Acanthopterygii; Percomosciaenidae; Pennahia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel.
MYOSIN HEAVY CHAIN.
Pennahia argentata.
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01-DEC-2001
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                            31 LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF------
                                                                                                   ETVDRLV-LESPAPVEVNLKLRRPSF
                                                                                                                                                                                                                                                                                  VAELGEQIDNLQRVKQKLEKEKSEYKMEIDDLSSNME-----AVAKAKGNLEKMCRTL
                                                                             EVEDLMIDVERANGLAANLDKKORNF
                                                                                                                             AQWRSKYETDAIQRTEELEEAKKKL--AQR-LQDAEEQIEAVNSKCASLEKTKQ--RLQS
                                                                                                                                                     FSSRSKLQT-----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVAS
                                                                                                                                                                               EELKR----QIEEEVKAKNALAHGVQSARHDCDLLREQFEEEQEAKAELQRGMSKANSEV
                                                                                                                                                                                                      ELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDL
                                                                                                                                                                                                                               EDQLSELKTKNDENVRQINDMSGQRARLLTENGEFTRQVEEKEALVSQLTRGKQAFTQQI 1307
                                                                                                                                                                                                                                                        KKQMKYLEQQQDE-
                                                                                                                                                                                                                                                                                                          ---LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL 135
                                                                                                                                                                                                                                                                                                                                    LEEISERLEEAGGATASQIEMNKKREAEFQKLRRDL---
                                                                                                                                                                                                                                                                                                                                                                                    ch 7.8%; l Similarity 23.3%; 76; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myosin_head
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16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW.
                                                                                                                                                                                                                                                                                                                                                                                    Score 185.5;
Pred. No. 0.04
63; Mismatches
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Last sequence up
Last annotation
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7.043;
                                                                                                                                                                                                                                                       -TKQAQEEAGRL----RSKMKTMEQI
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Euteleostei;
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on update)
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Neoteleostei;
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Matches 65
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01-MAY-1997
01-DEC-2001
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Caenorhabditis.
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B0432.9.
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EMBL; U80836; AAB37893.1; -.
InterPro: IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART: SM00184: RTNC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Farsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P., Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henkhaus J., Wohldmann P.; "The sequence of C. elegans Submitted (JAN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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 398
                                                                                    173
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                                                                                                                                                                                                                                 188
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                                                                                                                                                                                                                                              .2 Mb of contiguous nucleotide
                                                                                                                                     TVVSLQQAL----GKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELL
                                                                                                                                                                                       FFDL-----AQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNA
                                                                                                                                                                                                                              LQGSCSICFEDLKQNDKISAIVCGHIYHHGCISQWIAT--KRQCPSCRRTVPKNGFVEKL
                                                                                                                                                                        FFDVQRMGGEAEKPPEIDYRE-----EHYKLSTSLKVEQEK-----LGTLNTENKNLKD
                         DLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKK
                                                                                  LQSQLPEVEEMIRDMGVGQSAVEQLAVYC-----VSLKKEYENLKEARKASGEVADKLRK
                                                                                                             TVKSLEKKIIREKDKYRQEIPKLQATINHLTISSEETAYLKRELQESKNRLKTCEFYKIL
                                                                                                                                                                                                                                                                                          65; Conserv
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7 (TrEMBLrel.
1 (TrEMBLrel.
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AAKEIEQLKMEVQS----LKRAAQEDAAIKK
                                                                                                                                                                                                                                                                                                    7.6%;
                                                      -SSEADKQLGEYLKKNGNLDTEKFFQLMKSTNK---
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19,
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Last sequence
Last anno
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EMBL/GenBank/DDBJ
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Pred. No. 0.013;
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424
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RESULT Q9AV25

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RESULT O42352

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Best Local :
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBA0001014 genomic sequence.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC025783; AAK20041.1;
SEQUENCE 1578 AA; 178947 MW; CBB7E1DB68A821A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AV25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Oryza sativa (Rice)
                                                                                                                                                                                            1063
                                                                                                                                                                                                                                                          1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVEAQKVELKLQMDESRSLITNLKDELEQVEAQKVELKLQMDESRSLITNLKDELEQVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKR-----DSQVIIDTLRDTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKL----EHENVELSEF----ISGLESQLTYLANEKELSMLQMDESRSLITNLKDELE
EISAQTKLVMLGD----
                              -LGGRTKFIQPTDTVMIRPLPVKPKTKV
                                                                                           EELVGAFPI - - - - FVRNAILGQKQPKRPRSES
                                                                                                                                                           T----PPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPD
                                                                                                                                                                                                                          RLVLESPAPVEVNLK - - - -
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                                                                                                                                                                                                                                                                                        ----LDQAKLELKSAQK----DLQSADKEIMSLKKKLTMLQETLNLPPVASETVD-----
                                                                                                                                                                                                                                                                                                                                                                                      QKVELKENQLESHRRLSEVQEDSEALRRSNAKLQATVDHVVEECKSLQTLTADLKKQKLE
                                                             EVLTLQSSLDEAKFEKGKLEGLIQSLSEECEELKAQKGMLTDKVSCMQDTLNAANEGKQI
                                                                                                                           NMRRSIEAAR--SNEDNLRKTLCELELKSKSSDYEKQ--QIIEEISVLKIQVHKIAGLQD
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21.7%;
EP-PVKETSDV
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yta; Liliopsida;
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a; Poales; Poaceae;
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Best Local S
Matches 92
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Ol-JAN 1998 (TERMBLTEL 05, Last sequence
Ol-DEC-2001 (TERMBLTEL 19, Last annotatic
MYOSIN HEAVY CHAIN.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; E:
Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001609; myosin_head.
InterPro; IPR004009; myosin_N.
InterPro; IPR004009; myosin_Lail.
Pfam; PF00612; IQ; 2.
Pfam; PF00736; myosin_head; 1.
Pfam; PF00736; Myosin_N; 1.
Pfam; PF001576; Myosin_Lail; 1.
Pfam; PF01576; Myosin_Lail; 1.
Pram; PF001576; Myosin_Lail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00015; IQ; 1.
SMART; SM00015; IQ; 1.
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01-JAN-1998
01-JAN-1998
01-DEC-2001
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"Structural differences in the crossbridge hea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-FAST MUSCLE;
MEDLINE-97352533; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle."
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                         GOSCAGEPDEELV
                                                                                                                                   DRLV-LESPAPVEVNLKLRRPSFRDDI----
                                                                                                                                                                                      RSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETV
                                                                                                                                                                                                                                                                                                                            VAELGEQIDNLQRVKQKLEKEKSEYKMEIDDLTSNME-----AVAKAKGNLEKMCRTL
                                                                                                                                                                                                                                                                                                                                                                                LEEISERLEEAGGATAAQIEMNKKREADFQKMRRDL---EESTLQHEATAAALRKKQADT
                                                                                                                                                                                                                                                                                                                                                                                                         LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF-------
                                                  NSYEEALDHLETLKRENKNLQQEISDLSEQLGETGKSIHELEKAKKIVESEKAEIQTALE
                                                                            HGYYEKL----CLEKSHSPIQ------
                                                                                                        DLMIDGERANALAANLDKKQRNF-DKVLAEWKQKYEESQAELEAAQKEARSLSTELFKMK
                                                                                                                                                           RAKYETDAIQRTEELEEAKKKL--AQR-LQDAEESIEAVSSKCASLEKTKQ--RLQGEVE
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                                                                                                                                                                                                                                          -----EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSS
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D89991; BAA22068.1; -
P13538; 2MYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                          382
                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 181; DB 13; 21.2%; Pred. No. 0.075; ive 80; Mismatches 163;
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05, Last sequence update)
19, Last annotation update)
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Euteleostei;
                                                                                                                                 -DLNATFDVDTPPARPSSSQ-----
                                                                             -----DVPKKICKGPRKESQLSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     163;
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; Ostariophysi;
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Best Local
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Pfam; PF00063; myosin_N; 1.
Pfam; PF02736; Myosin_Tail; 1.
Pfam; PF01576; Myosin_Tail; 1.
PF101579; PF00193; MYOSINHEAVY.
PRINTS; PF00194; TROPOMYOSIN.
PT0D0m; PD000355; myosin_head; 1
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01-MAY-1999
01-MAY-1999
01-DEC-2001
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SMART; SM00242; MYSC; 1.

PROSITE; PS001225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1.

PROSITE; PS00186; IQ; 1.

PROSITE; PS50096; IQ; 1.

SEQUENCE 1958 AA; 224857 MW; 3FE254327DF89524
                                                                                        1108
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1168 KR
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Eukaryota; Metazoa; Platyhelminthes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYOSIN HEAVY CHAIN DJMHC-A.
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Paludicola; Dugesiidae;
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                                             306
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                                                                                                                                                                                 IETELKQTQETVDDLERVKRELEEQLKRKEMELSNASSKIEDESGLVAQLQKKIKELQAR
                                                                                                                                                                                                                              LFSSRSKLQTVYSELDQAKLE----LKSAQKDLQSA---
                                                                                                                                                                                                                                                                                                    IELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKD
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                                                                                        IQELEEDLEAERQARAKAEKSRHQLEGELEELSDRLEEQGGATSAQLELNKKREAELLKL
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Myosin_tail
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Last annotation updat
                                                                                                                                   NLPPVASETVDRLVLE - - - SPAPVEVN - - - - - - LKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 181;
Pred. No. 0.
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AC Q9034
AC Q903C
AC Q90
AC Q9
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Best Local S
Matches 68
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Q9Y577;
01-NOV-1999
01-NOV-1999
01-DEC-2001
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Q90338;
Q1-NOV-1996
Q1-JAN-1998
Q1-DEC-2001
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MEDLINE-97176447; PubMed-9023993;

Imal J., Hirayama Y., Kikuchi K., Kakinuma
"CDNA cloning of myosin heavy chain isoform
muscle and their gene expression associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
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J. Exp. Biol. 200:27-34(1997).
EMBL; D50475; BAA09068.1; -.
InterPro: IPR002928; Myosin_tail.
InterPro: IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygil; Neopterygil; Teleostei;
Cypriniformes; Cyprinidae; Cyprinus.
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01-JAN-1998 (TrEMBLrel. 05, L
01-DEC-2001 (TrEMBLrel. 19, L
MYOSIN HEAVY CHAIN (FRAGMENT)
TISSUE-TESTIS;
TISSUE-TESTIS;
MEDLINE-99011410; PubMed-9792805;
Ogawa S., Goto W., Orimo A., Hoso
Inoue S.;
                                                                                                                                                                                                                       RING
                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                NCBI_TaxID=9606;
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OV-1999 (TrEMBLrel. 12,
EC-2001 (TrEMBLrel. 19,
FINGER PROTEIN TERF.
                                                                                                                                                                                                                                                                                                                                                                                                                                            RAKYETDAIQRTEELEEAKKKL--AQR-LQDAEESIEAVSSKCASLEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET
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                                                                                                                                                       Chordata;
Primates;
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                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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Last annotation
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Pred. No. 0.046;
7; Mismatches 1
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                         Hosoi
                                                                                                                                                     Craniata; V
Catarrhini;
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                         T.,
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                         Ouchi
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Euteleostei;
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                                                                                                                                                       Hominidae;
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; Ostariophysi;
                                                                                                                                                                            Euteleostomi;
                                                                                                                                                       Homo
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Best Local
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                                                                                           Q22276 PRELIMINARY;
Q22276; Q22294;
Q1-NOV-1996 (TREMBLIEL 0
01-MAY-1999 (TREMBLIEL 1
01-MAY-2000 (TREMBLIEL 1
                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00622; SPRY; 1.

Pfam; PF00643; zf-B-DOX; 1.

Pfam; PF00097; zf-C3HC4; 1.

PRINTS; PR01406; BBOXZNFINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ogawa S., Inoue S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003878;
InterPro; IPR000315;
InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: CONTAINS 1 RING-TYPE EMBL; AF156271; AAD$40286.1; -IRR001870; Gamma_carbxylse.InterPro; IPR003877; SPRY.
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SEQUENCE '
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          SEQUENCE
                                                                                    T07C4.10 PROTEIN
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D.,
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                                                                                                                                                                                                                  VDRLVLESPAPVEVNLKLRRPSFRDDIDLNAT
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                                                                                                                                                                                                                                                    FSSRSKLQTVYSELDQAKLELKSAQKDLQSAD--KEIMSLKKKLTMLQETLNLPPVASET
                                                                                                                                                                                                                                                                                  ERIVLE-
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                                                                                                                                                                                                                                                                                                     ELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDL
                                                                                                                                                                                                                                                                                                                            EHRLHRVLPAEEAVQGYKL---KLEEDMEYLREQITRTGNLQAREEQSLAEWQGKVKERR
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$M00184; RING; 1.
$M00449; $PRY; 1.
E; P$00518; ZINC_FINGER_C3HC4;
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Berks
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                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
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Znf_bbox.
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Last sequence
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 179;
Pred. No. 0.
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                                                                                              sequence u annotation
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Best Loc
Matches
                                                                                                                                                                                                                                                           Q91411 PRELIMINARY; PRT; 764 AA. Q91411; 01-NOV-1996 (TrEMBLrel 01, Created) 01-NOV-1996 (TrEMBLrel 01, Last sequence update) 01-DEC-2001 (TrEMBLrel 19, Last annotation update) MYOSIN HEAVY CHAIN (FRAGMENT).
AMHCI Gallus gallus (Chicken).
 NON_TER
SEQUENCE
                      EMBL; $78540; AAB34772.2;
InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                            TISSUE-HEART ATRIUM;
MEDLINE-95324374; PubMed-7600964;
Yutzey K.E., Rhee J.T., Bader D.;
"Expression of the atrial-specific
                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1996) to the EMBL/
EMBL; Z48055; CAA88136.1; -.
EMBL; Z29443; CAA88136.1; JOINED.
EMBL; Z29443; CAA82580.1; -.
EMBL; Z48055; CAA82580.1; JOINED.
SEQUENCE 1138 AA; 132785 MW;
                                                                                         Development 120:871-883(1994).
                                                                                                        heart."
                                                                                                                  establishment of anteroposterior
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                          NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                      LMVSPEVSLVSEAPSSL-QDSRRSSHL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             LCLEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPDEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSS---QHGYYEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INLKNELDEMAVKLRNSQHQVAGLNEKISEEKRRKKQDADV----TRLDEQNQKL--
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90; Conservative
  764 AA;
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  88869 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 179; DB
Pred. No. 0.05
65; Mismatches
                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LDGRIEGYIRSEAAANNELERLRKDTAEQKEKLEA
 35AC9C64967FD1C2 CRC64;
                                                                                                                 ic myosin polarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                 heavy chain AMHC1 in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145;
                                                                                                                                                                                                                                                                                                                                                                                                                     844
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                                                                                                                               and
                                                                                                                  chicken
                                                                                                                             the
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RESULT
Q9WV59
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Best Local
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                InterPro; IPR003878; SPRY_dom
InterPro; IPR000315; Znf_bbox
InterPro; IPR001841; Znf_ring
Pfam; PF00622; SPRY; 1.
Pfam; PF00643; Zf-B_box; 1.
Pfam; PF00643; Zf-3HC4; 1.
                                                                                                              Submitted (JUN-1999) to the EMBL/GenE-!- SIMILARITY: CONTAINS 1 RING-TYPE EMBL; AF156272; AAD40287.1; -. HSSP; P15919; 1RMD.
                                                                                                                                                                                                                                                                                                                                                                                                                        Q9WV59;
                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE-TESTIS;
                                                                                                                                                                                                                                                                  Ogawa S.,
                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, RING FINGER PROTEIN TERF.
                                                                                                                                                                         Ogawa S., Goto W., Orimo
                                                                                                                                                                                                                     protein, terf, expressed in the testis.";
Biochem. Biophys. Res. Commun. 251:515-519(1998
                                                                                                                                                                                                                                                                   MEDLINE=99011410; I
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=TESTIS;
          PRINTS;
                                                                                         InterPro;
                                                                                                     InterPro;
                                                                                                                                                              Inoue S.
                                                                                                                                                                                                                                             "Molecular cloning of a novel RING finger-B
                                                                                                                                                                                                                                                           Inoue S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGRLRSKMKT-----MEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHRLQNEVEDLMADVERSNAAAAALDKKQRNFDKILSEWK---QKFEESQTELEASQKEA
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SM00336;
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                                                                                         IPR001870;
IPR003877;
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          BBOXZNFINGER
                                                                                                                                                                                                                                                                  PubMed=9792805;
Orimo A., Hosoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412
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                                                                                         SPRY
                                                                                                   Gamma_carbxylse
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23.1%;
                                                                Znf_bbox
                                                                              SPRY_domain.
                                                      Znf_ring
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Last
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                                                                                                                                                                         Hosoi T.,
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Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                       FINGER
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RESULT
Q9UIK7
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Best Local S
Matches 86
                                                                                                                                    Query Match
Best Local
                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                   Q9UIK7;
Q9UIK7;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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SMART; SM00449; SPRY; 1.
PROSITE; PS00518; ZINC_FINGER_C3HC4;
ZINC_FINGER_C3HC4;
SECTION CO.
                                                                                                                                                                           "Fusion of a Novel Gene, ELKS, to c-ret in a F
Carcinoma.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
EMBL; A8015617; BAA88763.1; -.
InterPro; IPR002017; Spectrin.
SEQUENCE 948 AA; 108792 MW; 344297FDFC9F7
                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                          Nakata T.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                          511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRTI; INKLF - - - FDLAQEEENVLDREFLKNELDNVRAQLSQKDKE - - - KRDSQVIIDTL
                                                                                              TICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVG-----KRTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVAIKTVCRV----PGQIEV-LK----SFQEDV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVASETVDRLVLESPAPVEVNLKLRRPSFRDDI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYL--EQQQDETKQAQEEAGRLRSKMKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCSICLDYF---TDPVMTACGHNFCRECIQMSWEKGKKKKKKKKKKKKKKKCKGSFPCPECREMSP
 VIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRS
                        \tt NKKTKQIQDMAEEKGTQAGEIHDLKDMLDVKERKVNVLQKKIENLQEQLRDKEKQMSSLK
                                                N---KLFFDLAQEE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKDLFSSRSKLQTVYSELDQAKLEL--KSAQKDLQSAD--KEIMSLKKKLTMLQETLNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KERRERILE----EFQKVVLFL-----VEEERRLLQILKKEED
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98
                                                                                                                                    Similarity
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0 (TrEMBLrel. 13,
1 (TrEMBLrel. 17,
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                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                    7.4%;
20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%;
                                       ----ENVLDRE-----FLKNELDNVRAQLSQKDKEKRDSQ
                                                                                                                        8O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                       HIEVLKESL-TAKEQRAAILQTEVDALRLRLEEKETML
                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                   Score 177.5; DE Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1AAB42BB02615ADF
                                                                                                                       Mismatches 135;
                                                                                                                                                                                   344297FDFC9F7602
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.024;
                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA
                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114;
                                                                                                                                                                                                                                              Papillary Thyroid
                                                                                                                                                                                                                     databases
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                                                                                                                                                                                   CRC64;
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                                                                                                                                              Length
                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                       111;
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                                                                                                                      Gaps
  161
                                               101
                                                                       510
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           Lightning J.;
Submitted (JUN-1994) to the EMBL/G
EMBL; Z34801; CAA84332.1; -.
EMBL; Z366514; CAA84332.1; JOINED.
EMBL; Z66514; CAA91344.1; -.
EMBL; Z34601; CAA91344.1; JOINED.
InterPro, IPR000237; GRIP.
Pfam; PF01465; GRIP; 1.
SEQUENCE 1133 AA; 129239 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q21022; Q21071;
01-NOV-1996 (TrEMBLrel. 01,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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 348
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                          284
                                                      288
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                                                                                                                                                                                                                                                                                                                                          Local Sir
hes 102;
                                                                                                                                                                                                                                                       90
                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                            46 CPQCRIQVGK----RTIINKLFFDLAQEEENV-----LDREFLKNELDNVRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SLKKEYENLKEARKASGEVADK---LRKDLFSSRSKLQTVYSELDQAKLELKSAQKD
                                                                                                                                                                   VSKKLDSSETSLKEFSDMIEAMKIQLINCEKQKDEAVELLKQ-KLEEVEKNMSDVEVQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNDKDKKIAELESLTSRQVKDQNKKVANLKHKEQVEKKKSAQMLEEARRREDNLNDSSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESQLKKAHEAALEAR-ASPEMSDRIQHLEREITRYKDESSKAQAEVDRLLEILKEVENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLKDLKEKVSLLQGDLSEKEASLLDLKEHASSLASSGLKKDSRLKTLEIALEQKKEECLK 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERVKSLQADTTNTDTALTTLEEALAEKERTIERLK-----EQRDRDEREKQEEIDNYKK
                                                                                                                                                                                             LEQOQDETKQAQEEAGRLRSKMKTM------EQIELLLQSQLPEVEEMIRDMGVGQ-
                                                                                                                                                                                                                           QLAKAMEKLNSEQNILDEVTKKLEQSEEEVLAARGAIQELTEKLEESEKETSTAKTELEA
                                                                                                                                                                                                                                                    LSQKDKEKRDS-QVIIDTLRDTLEERNATVVS-----LQQALGKAEMLCSTLKKQMKY
                                                                                                                                                                                                                                                                                   CDALQAEVNEAKALREEIQAKYDDVTQKAERIQGELEESKKVLESEKQAFENEKEQEREE
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 AKSTEDE --
                         ASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLE
                                                     SSAISEITKQMEAAKKELEASEKEKSELREQMDRLQKVHNAGQEDIQKLQKTWELEMAKI
                                                                                                             LLLESTTSEMKQHAEAAEIVKKQ---LEEAQSS----IENLKKDAENERN-LKTALESDE
                                                                                -SELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET----
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                           SAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY----
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      7.4%; Score 177.5; DE 20.5%; Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the EMBL/GenBank/DDBJ
KLAREQLAGELE-NAKEDL----
                                                                                                                                                                                                                                                                                                                                            103;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                      DB
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                                                                                 -LNLPPV
KVVEE
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ID Q9

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DT Q1

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Q9FJ35;
Q9FJ35;
Q9FJ35;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyle
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Sequence features of the regions of 1,013,767
physically assigned pl and TAC clones.";
DNA Res. 5:297-308(1998).
EMBL; AB016871; BAB10654.1; -.
SEQUENCE 1305 AA; 149961 MW; F37284B8E7BBF
          1239
                                                                                                                                                                                                                                                                                        1121
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MEDLINE-99087489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
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                                                                                                                                                                                                                                                                             LSNOKLRVTEQVLTEKEEAFRKEEAKHLEEQALLEKNLTMTHETYRGMIKEIADKVNITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRTIINKLEEDLAQEEENVLDR----EFLKN---ELDNVRAQLSQKDKEKRDSQVIIDT
       LGGKVREDEKEKEM-
                                                                                                                                          DGFQSMSEKLTEKQGRYEKTVMEASKILWTATNWVIERNHEKEKMNKEIEK--
                                                                                                                                                                               DVDTPPARPSSSQHGYYEKLCLEKS----
                                                                                                                                                                                                                                                                                                                                                      SLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRPSFRDDI-----DLNATF
                                                                                                                                                                                                                                                                                                                                                                                                                            VDYKEAQRLLEERGKEVTSRDSTIGVHEETMESLRNELEMKGDEIETLMEKISNIEVKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTM
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                                                                 LGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVVRTGFDGLGGRTKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KD-----LFSSRSK--------LQTVYSELDQAKLELKSAQKDLQSADKEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-----LSNQITDVQKAL------VEQEAAY-NTLEEEHKQINELFKETEATLNKVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y., Sato
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S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.4%;
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MKETLMGLGEEKREAIRQLC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 177.5; 1
Pred. No. 0.070
93; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 10;
.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162;
                                                                                                                                                                                                            HSPIQDVPKKICKGPRKESQLS
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7 bp covered
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   -VWIDHHRSRCEYL
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                                                                                                                                          KDEEIKK
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Best Local S
Matches 74
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Q90337;
                                           1252
                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Exp. Biol. 200:27-34(19 EMBL; D8990) BAA22067.1; EMBL; D50474; BAA09067.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-FAST SKELDTAL MUSCLE;
MEDLINE-9735253; PubMed-9208928;
Hirayama Y., Watabe S.;
"Structural differences in the crossbridge head of
associated myosin subfragment-1 isoforms from carp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cyprihiformes; Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acclimation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97176447; PubMed=9023993;
Imai J., Hirayama Y., Kikuchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=FAST SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004009; InterPro; IPR002928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem.
    179
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                                                                                                                                                                           79
                                                                                                                                                                                                                                                                 31 LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                           EDQLSEIKAKSDENSRQLNDMNAQRARLQTENGEFSRQLEEKEALV-SQLTRGKQAFTQQ
                                                                                    KKQMKYLEQQQDETKQAQEEAGRLRSKMKT---
                                                                                                                               VAELGEQIDNLQRIKQKLEKEKSEYKMEIDDLSSNME-----AVAKAKGNLEKMCRTL
                                                                                                                                                                                                                      LEEISERLEEAGGATAAQIEMNKKREAEFQKMRRDL---EESTLQHEATAAALRKKQADS
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                                                                                                                                                                           --- LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PD00035;
; SM00015; IQ; 1.
; SM000142; MYSC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00612; IQ; 1.
PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---EEVLSKTVVARGQRRVSQR
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                                                                                                                                                                                                                                                                                                             Similarity
74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001609;
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EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSS
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                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of myosin heavy chain isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200:27-34(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin_tail
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                                                                                                                                                                                                                                                                                                                                                                                                                        221092 MW;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                      Score 177.5;
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                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                 No. 0.12;
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Euteleostei; Ostariophysi;
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                                                                                  --MEQIELLLQSQLP----
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Matches 107
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Q9YHD8;
Q1-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thyroid Hormone-induced Metamorphosing Dev. Genet. 0:0-0(1999).

EMBL; AF097904; AAD13769.1; -.

InterPro; IPR002728; Myosin_tail.

InterPro; IPR000333; Tropomyosin.

Pfam; PF01576; Myosin_tail; 1.

PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE; Hu H., Merrifield P., Atkinson B.G.; "Expression of the Myosin Heavy Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana catesbeiana (Bull frog).
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYOSIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                          QMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQL
                                                                                                                                                                                                                                                                                                                                      TAQRARLQTENGELSRQL-----EEKESLITQLSRGKQAFTQQTEELRRQLEEETKAKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRLV-LESPAPVEVNLKLRRPSF
                                                                                LNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVD----TPPARPSSSQ
                                                                                                            KNLQQEISDLTEQISETGKTVHELEKAKKLVEQEKSDLQAALEEAEGSLEHEESKILRIQ
                                                                                                                                                                  DKKQRNEDKVLAEWKQKYEEAQAELESALKDARSMSTEIFKMKNAYEESLDQLETLKREN
                                                                                                                                                                                                                           AKKKLAQRLQE---AEEQVEAVNSKCASLEKTKQRLQA---EVEDLMVDVERSNSAAAAL
                                                                                                                                                                                                                                                                               LAHALQSSRHDCDLLREQYEEEQEAKAELQRALSKANSEVAQWRTKYETDAIQRTEELEE
                                                                                                                                                                                                                                                                                                          ----RDSQVIIDTLRDTLEERNATVVSLQQALGKAE-----
                                                                                                                                                                                                                                                                                                                                                                  TCPQCRIQVGKRTIINKLFFDLAQEEENVL----DREFLKNELDNVRAQLSQKDKEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLMIDGERANALAANLDKKQRNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETV
EGDLNELETQLSHANRQAAEAQKQLRNVQAHLKDNQLQLDD---ALRSQEDLKEQVAVVE
                                                                                                                                                                                               -----AVYCVSLKKEYEN-----LKEARKASGEV-----ADKLR-----
                        HGYYEKLCLEKSHSPIQ--DVPKKI--CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFV
                                                                                                                                                                                                                                                                                                                                                                                              al Similarity 22.8
107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   879 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence up
(TrEMBLrel. 17, Last annotation
                                                                                                                                        -KDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIM-SLK-KKLTMLQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101710 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             7.4%;
                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                            Score 177; DB 13;
Pred. No. 0.053;
82; Mismatches 184,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1C456851E968A3D8 CRC64;
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Grana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                               184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the Tail catesbeiana
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                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muscle of Tadpoles.";
                                                                                                                                                                                                                                                                                                                                                                                              96;
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Best Local :
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01-JAN-1998
01-JUN-2001
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SEQUENCE FROM N.A.
Monier S., Janouelx-Lerosey I
                                                                                                                                             028714
028714;
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EMBL; AF340028; AAK26381.1; -.
InterPro; IPR002017; Spectrin.
InterPro; IPR00533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 976 AA; 111931 MW; 4
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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                                                 CHROMOSOME SEGREGATION
                           AF1558
                                                                                                                                                                                                                                                                                         832
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                                                                                                                                                                                                                                                                                                                                        291 LVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEK
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                                                                                                                                                                                                                                                                                         LQVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                    LQSADKEIMSL--
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Rodentia;
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Sciurognathi;
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Archaeoglobus fulgidus

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Matches
                               066878 PRELIMINARY;
066878;
01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
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Klenk H.-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E.,

Klenk H.-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Kirkness E.F., Ougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
           CHROMOSOME ASSEMBLY XCPC OR AQ_629
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003439; ABC_transportr.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
InterPro; IPR00317; Spectrin.
Pfam; PF02483; SMC_C; 1.
Pfam; PF02483; SMC_N; 1.
PFROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome. SEQUENCE 1156 AA; 134244 MW; 18CB16F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; AF1558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).
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Archaeoglobus.
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                                                                                                                                                                                                                 TIEEGKARVEEINSELEELRKEERELGKELKGLRKERDELIKQLRNAEEEKRKIEAEIDR
                                                                                                                                                                                                                                                                                                                                            KERMLSDKIYELQREKEGLFAELNRAESLRKQYKDEVDRLTGMISELRNRISLLDEKIRT
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                                                                                                                                                   RRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQD
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                       PROTEIN
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21.48;
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                      Last sec
Last anr
HOMOLOG.
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                                          update)
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InterPro;
 SEQUENCE
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
MYOSIN HEAVY CHAIN 2X.
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaastrand T., Young W.G., Le Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392:353-358(1998)
EMBL; AE000699; AAC06839
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NCBI_TaxID=63363;
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srPro; IPR003487; ATP_GTP_A.
srPro; IPR003716; RNA_pol_omega.
srPro; IPR003405; SMC_C.
erPro; IPR003395; SMC_N.
erPro; IPR003395; SMC_N.
erPro; IPR002317; Spectrin.
m; PF02483; SMC_N; 1.
srTE; PS00211; ABC_TRANSPORTER; UNI
                                                                                                                                                                                                                                                                                                      KRMNLGRESFIPLNRVRVEERPLRYPRTKGA
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l Similarity 22.0%;
86; Conservative 8
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                                                    Chordata; Crania:
Cetartiodactyla;
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19,
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                                                                                                                            Created)
Last sequence
Last annotation
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Pred. No. 0.08
88; Mismatches
                                                    Craniata; Veri
actyla; Suina;
                                                                                                                              sequence up
annotation
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                                                      Vertebrata;
ina; Suidae;
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                                                        Euteleostomi;
Sus.
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Huber
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                               D Q98TQ6 PRELIMINARY; PRT; 1929 AA.
C Q98TQ6;
C Q98TQ6;
T 01-JUN-2001 (TrEMBLrel. 17, Created)
T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E MYOSIN HEAVY CHAIN.
N MYOSIN HEAVY CHAIN.
S Notothenia coriiceps (black rockcod).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
C Eukaryota; Metazoa; Chordata; Craniata; Perciformes;
C Actinopterygii; Neopterygii; Percomorpha; Perciformes;
C Notothenidae; Notothenidae; Notothenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head
InterPro; IPR004009; Myosin_N.
InterPro; IPR004009; Myosin_tail
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00736; Myosin_N; 1.
Pfam; PF00736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINLEAVY.
ProDom; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain-2a, -2x, and -2b isoforms.";
Meat Sci. 57:311-317(2001).
EMBL; AB025262; BAA82146.1; -.
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SEQUENCE FROM N.A
                     NCBI_TaxID=8208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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; SM00242; MYSC; 1
; SM002496; IQ; 1
                                                                                                                                                                                                                                                                      EVEDLMIDVERSNAACAALDKKQRNF-DKILAEWKQKYEETHAELEASQKESRSLSTELF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87; Conservative
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IQ; 1.
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Myosin_N.
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                                                                     Euteleostomi;
                                                          Neoteleostei;
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Best Local
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01-MAY-2000
01-MAY-2000
01-JUN-2001
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SMART; SN
SEQUENCE
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EMBL; AJ243767; CAC27776.1; -.

HSSP; P13538; 2MYS.
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                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
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pfam; PF02736; Myosin_N; 1.
pfam; PF01576; Myosin_tail; 1.
prINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
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           EMBL; AF194970; APMGD; MGI:1915046;
                         LEK/centromere protein F/mitosin gene
J. Biol. Chem. 274:18597-18604(1999).
EMBL; AF194970; AAF707196.1;
                                                                        "The
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InterPro; IPR004009;
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 NON_TER
                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99303627; PubMed=10373470;
                                                                                                                                                                                      Mus musculus (Mouse).
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                                                     win R.L., Pabon-Pena L.M., Foster G.C., Bader D.; cloning and analysis of LEK1 identifies variations centromere protein F/mitosin gene family.";
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                                                                                                                                                                                                               (FRAGMENT).
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; SM00015; IQ
; SM00242; MY
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Pred. No. 0.
                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
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044929;
01-JUN-1998 (TrEMBLrel. 06, C.
01-JUN-1998 (TrEMBLrel. 17, L.
01-JUN-2001 (TrEMBLrel. 17, L.
MICROTUBULE BINDING PROTEIN D
CLIP-190 OR CG5020.
                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                    FlyBase; FBqn0020503; CLIP-190.
InterPro; IR000938; CAP-GLY.
Pfam; PF01302; CAP-GLY; 2.
SEQUENCE 1690 AA; 189103 MW;
                                                                                                                                                                                                                                                                                                                     STRAIN-OREGON R;
Lantz V.A., Miller K.G.;
J. Cell Biol. 0:0-0(1998).
EMBL; AF041382; AAB96783.1;
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 NGSLEEEAKKSGQLQEQITKLKSEVEETQAALSSYHTDVESKTKQLEAANAALEKVNKEY
                         --NLKEARKASGEVAD---KLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEI
                                                  QVQLEQLQQQAAASGEEGSKTVAKLHDEISQLKSQAEETQSELKSTESNLEAKSKQLEAA
                                                                        E-QIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYE---
                                                                                                   QQQLEEKTLGHEKLQAAL-----EELKKEKETIIKEKEQELQQLQSKSAESESALKVV
                                                                                                                         RDTLEERNATVVSLQQALGKAEMLCSTLKKQMK-YLEQQQDETKQAQEEAGRLRSKMKTM
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; Pred. No. 0.2;
63; Mismatches
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Pred. No. 0.14
84; Mismatches
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a; Brachycera;
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Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human
The complete sequences of 100 new cDNA clones from brain w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TREMBLREL. 19, KIAA1081 PROTEIN (FRAGMENT).
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HSSP; P01100; 1
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                                                                                                                                                                                                                                              NKKVANLKHKEQVEKKKSAQMLEEARRREDNLNDSSQQLQDSLRKKDDRIEEL----
                                                                                                                                                 SDRIQHLEREITRYKDESSKAQAEVDRLLEILKEVENEKNDKDKKIAELESLTSRQVKDQ
                                                                                                                                                                                                                                                                                                                                                                                       ALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEVEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIEVLKESL-TAKEQRAAILQTEVDALRLRLEEKETMLNKKTKQIQDMAEEKGTQAGEIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLQCLIQSFETAPSRTCPQCRIQVG-----KRTIIN---KLFFDLAQEE------
SFRDDIDLNATFDV --
                                                                                                                                                                                                  ADK----LRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLKDMLDVKERKVNVLQKKIENLQEQLRDKEKQMSSLKERVKSLQADTTNTDTALTTLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ENVLDRE-----FLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAKTENLELSTGTQTTIKDLQERLE----ITNAELQHKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AESRAEASDLQDKV-----KEITDTLHAELQAERSSSSALHTKLSKFSDEIATGHKELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVN--LKLRRPSFRDDI-----DLN
                                                                                                                                                                                                                                                                                                                                                   ALAEKERTIERLK -----EQRDRDEREKQEEIDNYKKDLKDLKEKVSLLQGDLSEKEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKADAWSQEMLQKEKELQELRQQLQDSQDSQTKLKAEGERKEKSFEES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATEDV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity
86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAA83033.1; -.
                                                                                               KKKLTMLQETL----NLPPVASETVDRLVLESPAPVEVNLKLRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spectrin
-DTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 174.5; DB pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08D94249ACC63F22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n genes.
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361
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                                                                                                                                                                                                  267
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RESULT
Q9YHD4
ID Q9
AC Q9
DT 0:
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Best Local
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Q9YHD4
Q9YHD4;
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN (FRAGMENT).
Theragra chalcogramma.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Actinopterygii; Peracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR002928; Myosin_tail.
Interpro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-FAST MUSCLE;
Togashi M., Hirayama Y., Kakinuma M., Watabe
"cDNA cloning of Alaska polack fast skeletal
chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P87344;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB000214; BAA19070.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=48550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theragra.
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                                                                                                    604
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                                                                                                                                                            554
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                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                     LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF-------
                                                                                                                                                                                                                                                                                                                                 VAELGEQIDNLQRVKQKLEKEKSEFKMEIDDLSSNME-----AVSKAKGNLEKICRAL
                                                                                                                                                                                                                                                                                                                                                    ---LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KETHLT 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALRESVQITAEREMVLAQEESARTNAEKQVEELLMAMEKVKQELESMKAKLSSTQQSLAE
                                                                                                    RLQGEVEDLMVDVERANGLAANLDKKQRNF
                                                                                                                   PVASETVDRLV-LESPAPVEVNLKLRRPSF: | | :| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                          LEEISERLEEAGGATSAQIEMNKKREAEFQKLRRDL---EESTLQHEATAAALRKKQADS
                                                                                                                                                                                     RKDLFSSRSKLQT-----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLP
                                                                                                                                                                                                                   EELKRQNEEEVKAKNALAHGVQSARHDCDLLREQFEEEQEAKAELQRGMSKANGEVA---
                                                                                                                                                                                                                                              EEMIRDMGVGQSAVEQLA-----VYCVSLKKEYENLKEAR-----KASGEVADKL
                                                                                                                                                                                                                                                                           EDQLSEIKAKSDENARQVNDISAQRARLLTENGEFGRQLEEKEALVSQLTRGKQAYTQQV
                                                                                                                                                                                                                                                                                                      KKOMKYLEQQQDETKQAQEEAGRLRSKMKT-----MEQIELLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity 79; Conserv
                                                                                                                                                          -QWRSKYETDAIQRTEELEESKKKL--AQR-LQEAEEQIEAVNSKCASLEKTKQ--
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   (TrEMBLrel. 10,
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                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Mismatches
   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 174.5; DB Pred. No. 0.094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B8C5FECAE6F5B954
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                              A
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muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1119;
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RESULT
Q98TQ5
ID Q0
AC Q0
DT 00
DT 00
DT 00
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Best Local
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Q98TQ5;
Q98TQ5;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE;
Hu H., Merrifield P., Atkinson B.G.;
"Expression of the Myosin Heavy Chain Genes in the Tail Muscle
"Expression of the Myosin Heavy Chain Genes atesbeiana Tadpole"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thyroid Hormone-induced Metamorphosing Dev. Genet. 0:0-0(1999).
EMBL; AF099908; AAD13773.1; -.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                               478
                                                                                                                                                         462 KLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                     36
                                                                                                                               EVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATVVSLQQALGKAEMLCS-------TLKKQMKYLEQQQDETKQAQEEAGRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEKESLVSQLSRGKQAFTQQTEELKRQLEEETKAKNALAHALQSARHDCDLLREQYEEEQ
                                                                                                                                                                                     ALEQTERGRKVAEHELLDVTERVQLLHTQNTSLI-----NTKKKLEADV---
                                                                                                                                                                                                                                                                                                                                                            ESGKSIHETEKAKKQVEQEKSELQSALEEAEGSLEHEEAKILRVQLELNQVKSE-VDRKV
                                                                                                                                                                                                                                                                                                                                                                                                                     KYEEAQAELEAAQKESRGLSTEVF-KMKNNYEEALDQLETLKRENKNLQQEISDLTEQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KEARKASGEVADKLRKDLFSSRSKLQTV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKCASLEKTKQRLQA---EVEDLMVDVERSNSA-----CTALDKKQKNFYKVLSEWKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENL------
                                                                                                                                                                                                                  ---ESSCSKDVVRTGFDGLGGRTKFIQPTDTVMIRPLPVKPKTKVKQRVRVKTVPSLFQA
                                                                                                                                                                                                                                              RQAAEAQKQLRNVQGQFKDAQLHLDD----AIRGNDDLKEQLAIVERRNNLMQAEIEEMRS
                                                                                                                                                                                                                                                               IQ--DVPKKI--CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRS
                                                                                                                                                                                                                                                                                                      AEKDEEIE----QLKRNSQRALESMQTSLDSEVRSRNDALRLKKKMEGDLNEMEIQLSHAN
                                                                                                                                                                                                                                                                                                                               LESPAPVEVNLKLRRPSFRDDIDLNATFDVD----TPPARPSSSQHGYYEKLCLEKSHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAKAELQRSLSKANSEVSQWRTKYETDAIQRTEELEEAKKKLAQRLQE---AEEQIEAVN
                                                                                                                                                         464
                                                                                                                                                                                                                                                                                                                                                                                        -YSELDQAKLELKSAQKDLQSADKEIM-SLK-KKLTMLQETLNLPPVASETVDRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671 AA;
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.3%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78062 MW;
 17,
17,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
Last sequence up
                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 174; DB 1
Pred. No. 0.058;
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                                                         975
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               update)
update)
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89

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428 404 314 292 255 239

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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                096063;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Kobatashi C., Agata
Submitted (JUN-1998)
                                                                                                                                                                                      Dugesia japonica (Planarian).
Eukaryota; Metazoa; Platyhelminthes;
Paludicola; Dugesiidae; Dugesia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Notothenia coriiceps (black rockcod).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Peleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Notothenioidei; Nototheniidae; Notothenia.
       Kobayashi
                          SEQUENCE FROM N.A
                                                                                                                                                                  NCBI_TaxID=6161;
                                                                                                                                                                                                                                                                 ДЛМНС-В.
                                                                                                                                                                                                                                                                                                                                                                                                            096063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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MYOHC-A3 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELKR----QIEEEVKAKNALAHGLQSARHDCDLLREQFEEEQEAKAELQRGMSKANSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAELGEQIDNLQRVKQKLEKEKSEYKMEIDDLSSNME-----NVAKAKGNLEKMCRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVEDLMIDVERANALAANLDKKQRNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETVDRLV-LESPAPVEVNLKLRRPSF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQWRSKYETDAIQRTEELEESKKKL--AQR-LQEAEEQIEAVNSKCASLEKTKQ--RLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSSRSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDQFSELKTKNDENVRQINDTSSQKARLLTENGEFSRQVEEKEALVSQLTRGKQASTQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKQMKYLEQQQDE---------TKQAQEEAGRL----RSKMKTMEQI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEEISERLEEAGGATSAQIEMNKKREAEFQKLRRDL---EESTLQHEATASALRKKQADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
72; Conserv
       c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            975 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
       Kobayashi S.,
                                                                      ) K
to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%;
22.1%;
                                                                      Orii H.;
the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 173.5; DB; Pred. No. 0.092; 67; Mismatches 1
    Orii H.,
                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489
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    Agata
                                                                                                                                                                                                                 Turbellaria;
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                                                                        databases
    Watanabe K.;
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RESULT
Q9AMC4
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DE M1
GN EN

Q9AMC4

PRELIMINARY;

437 AA

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09AMC4; 01-JUN-2001 01-JUN-2001 01-DEC-2001

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

17, 17, 19,

Created)
Last sequence update)
Last annotation update)

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Best Local Similarity
Matches 94; Conserv
                                                                                                              1126
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head;
Pfam; PF01576; Myosin_tail;
1163 KSNSQGTGGVRSEEM----EEFKRKMNARIQELEEESESNKSKCSQLEKVKSRLQG
                                                                                                                                                                                                                        1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002928;
InterPro; IPR000533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001637;
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                                                                                                                                                                  307
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                                                                                                                                                                                                                                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      892
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                                                                                                                                                                                                                        QHENSELHKSLEDAESQINQLSKAKQQLQAQL-----EEAKQNLEDESRAKSKLNGDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDTLRDTLEERNATVVSLQ-----QALGKAEMLCSTLKKQMKYLEQQQDE---TKQAQ
                                                                                                                                                                                                                                                                                                                                 KNELRGDIEDLSGQLESLNKAKINLEKSNKGLEATISELQNKLDELTKQLSDAGNSNNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                    TDLNKKREAELMKLKRDLEEANMQHEQAIMQTRKKQQDTANEFADQLDQLQKSKSKIERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEKAKR----KVEGELKQNQEMLNDLERVKSELEE---QLKRKEMELNGANSKIEDENNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQVGKRTIINKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEK-----RDSQVI 103
                                                   SLGGQSCAGEPDEELVGAFPIFVR--NAILGQKQPKRPRSESSCSK-DVVRTGFDG
                                                                                                                                                                                                                                                                           KLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLR
                                                                                                                                                                                                                                                                                                                                                                                 MGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQA
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                                                                                                                                                            RPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQL
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PR00193; MYOSINHEAVY
PR00194; TROPOMYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000048;
IPR001609;
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IPR001637; GlnA_adenyltn.
IPR000524; HTH_GntR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNNI
                                                                                                            NALSDLDA - - MRES - - - - - -
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22.6%;
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Myosin_tail.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 173.5; D
Pred. No. 0.17;
'5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0D4A821FA6CFF7C2
                                                                                                            -----LEEEQEGKSDVQRQLVKVQNELQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
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  1214
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RESULT
Q99MI1
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Best Local
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Eshaghi M., Manaf A., Yusoff K., Jamal F.;

Eshaghi M., Manaf A., Yusoff K., Jamal F.;

"Sequence Analysis of the 5' Region of the emm

streptococci Isolates from Malaysia.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ

EMBL; AF326566; AAK11617.1;

InterPro; IPR001899; Gram_pos_anchor.

InterPro; IPR003345; M_repeat.
                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaria; Eutheria; Rodentia;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence up
01-DEC-2001 (TIEMBLRel. 19, Last annotation
RAB6-INTERACTING PROTEIN 2 ISOFORM B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0015; GPOSANCHOR.

PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02370; M; 9.
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
EMBL; AF340029; AAK26382.1; -.
InterPro; IPR002017; Spectrin,
SEQUENCE 1120 AA; 128330 MW; A542B526FAEDI
                                                                                                                                                                                                       Q99MI1;
01-JUN-2001
                                                                                                                                                                                                                                  Q99MI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
SEQUENCE 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes. Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1314;
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                                                   Rab6
                                                             "Characterization
                                                                           SEQUENCE FROM N.A.
                                                                             Monier
                                                                                                                                                                                                                                                                                                377
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                                                                                                                                                                                                                                                                                               PGKGQAPQAGTKPNQNKAPMKETKRQLPSTGEAANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQE-----EAGRLRSKM
                                                                                                                                                                                                                                                                                                                     LEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEP
                                                                                                                                                                                                                                                                                                                                               AEAKALKEQLAKQA---
                                                                                                                                                                                                                                                                                                                                                                      PVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLC
                                                                                                                                                                                                                                                                                                                                                                                                RQGLSRDLEASREVKKKVEADLAEANSKLSSPLKNLTKSLKKVRNYQKK-KKLSSSKRLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTMEQIELLLQSQLPEVEE--MIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLEKTVKDKIAREQ----KSKQDFGALNQELAKKEEQNKISDASRKGLRRDLDASREAKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LATQKEN-LEKEVVEAKHKNETLNINNDDLTKKLNETRQELANKQQESKENE---KTLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 77; Conserv
                                                             Janoueix-Lerosey ization of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 · AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                 / I., Julian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.0.
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 173;
Pred. No. 0
                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                  PRT;
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 A542B526FAEDF9C7
                                                                                                                                                                                                                                  1120
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                                                           partner
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; Murinae; Mus
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ACCOMPAND DESCRIPTION OF THE PROPERTY OF THE P
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Q9YHD7
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01-MAY-1999
01-DEC-2001
                                                                                                                                                                                                                                                           Thyroid Hormone induced Metamorphosing Dev. Genet. 0:0-0(1999).
EMBL; AF097905; AAD1370.1; -.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9YHD7;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=TAIL MUSCLE, HI
Hu H., Merrifield P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; V
Amphibia; Batrachia; Anura; Neobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9YHD7
                                                              y Match
: Local Similarity
Thes 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=TAIL MUSCLE, HINDLIMB MUSCLE;
Hu H., Merrifield P., Atkinson B.G.;
"Expression of the Myosin Heavy Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rana catesbeiana (Bull frog).
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                        NON_TER
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47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELESMKAKLSSTQQSLAEKETHLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MESQLKKAHEATLEAR-ASPEMSDRIQQLEREISRYKDESSKAQTEVDRLLEILKEVENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLKDLREKVSLLQGDLSEKEASLLDIKEHASSLASSGLKKDSRLKTLEIALEQKKEECLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMKTMEQIELLLQSQLPEVEEMIRDMGVGQS------AVEQLAVYCV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERVKSLQADTTNTDTALTTLEEALADKERTIERLK-----EQRDRDEREKQEEIDTYKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKKTKQIQDMAEEKGTQAGEIHDLKDMLDVKERKVNVLQKKIENLQEQLRDKEKQMSSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N---KLFFDLAQEE-----ENVLDRE-----FLKNELDNVRAQLSQKDKEKRDSQ 101
TTQRARLQTENGELSRQL----
                                     TCPQCRIQVGKRTIINKLFFDLAQEEENVLD-----REFLKNELDNVRAQLSQKDKEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVLESPAPVEVNLKLRRPSFRDDIDLNATFDV---DTPPARPSSSQHGYYEKLCLEKSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQSADKEIMSL------
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                                                                                                                                                                                                                                          PR00194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLKKEYENLKEARKASGEVADK---LRKDLFSSRSKLQTVYSELDQAKLELKSAQKD
                                                                                                                                                                                                 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TremBLrel. 10, Created)
(TremBLrel. 10, Last seq
(TremBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                   Α
                                                                                                                                                                                                                                          TROPOMYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%;
19.6%;
                                                                                                                                                                                                 81824 MW;
                                                                                                      7.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIEVLKESL-TAKEQRAAILQTEVDALRLRLEEKETML 538
EEKESLISQLSRGKLGFTQQVEELKRQLEEESKAKNA 101
                                                                                                    Score 172.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 173;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                 BE2D01700017BC4C
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                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          708
                                                                                                           0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
a; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
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                                                                                   142;
                                                                                                                                                                                                                                                                                                                                                                             in the Tail catesbeiana
                                                                                                                               13;
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                                                                                   Indels
                                                                                                                             Length
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Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                  Muscle
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                                                                                                                               708
                                                                                   91;
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                                                                                   Gaps
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                                                                                      19;
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B	οy	рь	γQ	дb	Qy	DЬ	Qy	Вb	Qy	Дb	Qy.
392	334	336	278	276	240	217	198	160	146	102	98
392 EGDLNELEIQLSHANRQASEAQKQLRNVQGQLKDTQLHL-DDAVRGQED 439	334 HGYYEKLCLEKSHSDIQDVPKKICKGPRKESQLSLGGQSCAGEPD 378	LELNQIKSE-VDRKIAEKDEEIEQLKRNSQRAIDTMQSTLDSEIRSRNDALRLKKKM 391	278 LNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQ 333	276 KNLQQEISDLTEQIGENGKSINELEKARKQVEQEKSDLQAALEEAEGSLEHEEAKILRVQ 335	240SELDQAKLELKSAQKDLQSADKEIM-SLK-KKLTMLQET 277	KKQRNFDKVLVEWKQKYEBGQAELEASQKEARSLSTEIF-KLKNSYEEALEQVETLKREN 275	AVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTV 239	160 EDAKKKLAQRLQDAEEQVEAVNSKCGSLEKTKQRLQSEVEDLMVDVERANGAAAALD 216	146 QDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQL- 197	102 LAHALQSSRHDNDLLREQYEEEQEAKAELQRSLSKANGEVAQWRTKYETDAIQRTEEL 159	98RDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQ 145

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